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xecuting TD287
Hilight option is not available in file(s) 398, 399
HILIGHT set on as '%'
          132189  NEISSERIA
           59916  MENINGITIDIS
      S1   57166  NEISSERIA (1W) MENINGITIDIS
? s s1 and fur (1w) gene
Processing
Processed  10 of  60 files ...
Processing
Processed  40 of  60 files ...
Completed processing all files
           57166  S1
         1108021  FUR
         8745398  GENE
            1647  FUR(1W)GENE
      S2      60  S1 AND FUR (1W) GENE
? rd
>>>Duplicate detection is not supported for File 398.
>>>Duplicate detection is not supported for File 654.
>>>Duplicate detection is not supported for File 349.
>>>Duplicate detection is not supported for File 348.
>>>Duplicate detection is not supported for File 340.
>>>Duplicate detection is not supported for File 174.
>>>Duplicate detection is not supported for File 447.
>>>Duplicate detection is not supported for File 345.
>>>Duplicate detection is not supported for File 342.
>>>Duplicate detection is not supported for File 761.
>>>Duplicate detection is not supported for File 70.
>>>Duplicate detection is not supported for File 128.
>>>Duplicate detection is not supported for File 449.
>>>Duplicate detection is not supported for File 107.
>>>Duplicate detection is not supported for File 286.
>>>Duplicate detection is not supported for File 446.
>>>Duplicate detection is not supported for File 429.
>>>Duplicate detection is not supported for File 459.
>>>Duplicate detection is not supported for File 229.

>>>Records from unsupported files will be retained in the RD set.
>>>Record 440:10925408 ignored; incomplete bibliographic data, not retained
 in RD set
>>>Record 440:5352096 ignored; incomplete bibliographic data, not retained
in RD set
>>>Record 440:4304990 ignored; incomplete bibliographic data, not retained
in RD set
>>>Record 440:3535442 ignored; incomplete bibliographic data, not retained
in RD set
...examined 50 records  (50)
...completed examining records
      S3      39  RD (unique items)
? t s3/3,ab/1-39
>>>No matching display code(s) found in file(s): 65, 107, 128-129, 135,
   229, 342, 345, 398, 429, 446-447, 449, 459, 761

 3/3,AB/1     (Item 1 from file: 73)
DIALOG(R)File  73:EMBASE
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12305539     EMBASE No: 2003411326
  The iron-responsive regulator Fur is transcriptionally autoregulated and
not essential in %Neisseria% %meningitidis%
  Delany I.; Ieva R.; Alaimo C.; Rappuoli R.; Scarlato V.
  V. Scarlato, Biochem. and Molecular Biology Unit, IRIS, Chiron S.r.l.,
  Via Fiorentina 1, 53100 Siena  Italy
  AUTHOR EMAIL: enzo scarlato@chiron.it
  Journal of Bacteriology ( J. BACTERIOL. ) (United States)   2003, 185/20
  (6032-6041)
  CODEN: JOBAA   ISSN: 0021-9193
  DOCUMENT TYPE: Journal ; Article
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after

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 39

Fur is a well-known iron-responsive repressor of gene transcription, which is used by many bacteria to respond to the low-iron environment that pathogens encounter during infection. The %fur% %gene% in %Neisseria% %meningitidis% has been described as an essential gene that may regulate a broad array of genes. We succeeded in obtaining an N. meningitidis mutant with the %fur% %gene% knocked out and used it to undertake studies of fur-mediated iron regulation. We show that expression of both Fur and the transferrin binding protein Tbp2 is iron regulated and demonstrate that this regulation is Fur mediated for the Tbp2 protein. Footprinting analysis revealed that Fur binds to two distinct sites upstream of its coding region with different affinities and that these binding sites overlap two promoters that differentially control transcription of the %fur% %gene% in response to iron. The presence of two independently regulated fur promoters may allow meningococcus to fine-tune expression of this regulator controlling iron homeostasis, possibly during infection.

3/3,AB/2 (Item 2 from file: 73)
DIALOG(R)File 73:EMBASE

05724381 EMBASE No: 1994118985
Cloning and sequence analysis of the %fur% %gene% encoding an iron-regulatory protein of %Neisseria% %meningitidis%
Karkhoff-Schweizer R.R.; Schryvers A.B.; Schweizer H.P.
Depart. Microbiol./Infectect. Dis., Univ. Calgary Hlth Sciences Center, 3330 Hospital Drive N.W.,Calgary, Alta. T2N 4N1 Canada
Gene (GENE) (Netherlands) 1994, 141/1 (139-140)
CODEN: GENED ISSN: 0378-1119
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The %fur% %gene%, encoding an iron-regulatory protein in %Neisseria% %meningitidis% strain B16B6, has been cloned and sequenced. Its product showed a high degree of homology to known Fur sequences.

3/3,AB/3 (Item 1 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

16922452 Document Delivery Available: 000185244400017 References: 31
TITLE: Molecular cloning and characterization of a 79-kDa iron-repressible outer-membrane protein of Moraxella bovis
AUTHOR(S): Kakuda T (REPRINT); Oishi D; Tsubaki S; Takai S
AUTHOR(S) E-MAIL: kakuda@vmas.kitasato-u.ac.jp
CORPORATE SOURCE: Kitasato Univ, Dept Anim Hyg, /Towada/Aomori 0348628/Japan/ (REPRINT); Kitasato Univ, Dept Anim Hyg, /Towada/Aomori 0348628/Japan/
PUBLICATION TYPE: JOURNAL
PUBLICATION: FEMS MICROBIOLOGY LETTERS, 2003, V225, N2 (AUG 29), P279-284
GENUINE ARTICLE#: 720CR
PUBLISHER: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS
ISSN: 0378-1097
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: Moraxella bovis expresses an iron-repressible 79-kDa outer-membrane protein, lrpA. DNA and N-terminal amino acid sequence analysis indicate that IrpA is closely related to FrpB of %Neisseria% %meningitidis%, FetA of Neisseria gonorrhoeae and CopB of Moraxella catarrhalis. The results of manganese mutagenesis and a gel-shift assay suggested that the transcription of irpA is negatively regulated by the ferric uptake regulator. The insertion of an antibiotic resistance cassette into the irpA gene affected the strain's ability to utilize bovine transferrin and lactoferrin. IrpA was detected in geographically diverse clinical isolates, and the antigenicity of lrpA was conserved in all the

isolates tested. Therefore, lrpA may have potential as a candidate vaccine.

3/3,AB/4 (Item 2 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

10591078 References: 37
TITLE: Genetic characterization of wild-type and mutant fur genes of Bordetella avium
AUTHOR(S): Murphy ER; Dickenson A; Militello KT; Connell TD (REPRINT)
AUTHOR(S) E-MAIL: connell@acsu.buffalo.edu
CORPORATE SOURCE: SUNY Buffalo, Sch Med & Biomed Sci, 3435 Main St,138 Farber Hall/Buffalo//NY/14214 (REPRINT); SUNY Buffalo, Sch Med & Biomed Sci, /Buffalo//NY/14214; SUNY Buffalo, Sch Med & Biomed Sci, /Buffalo//NY/14214
PUBLICATION TYPE: JOURNAL
PUBLICATION: INFECTION AND IMMUNITY, 1999 V67, N6 (JUN), P3160-3165
GENUINE ARTICLE#: 199GX
PUBLISHER: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW, WASHINGTON, DC 20005-4171 USA
ISSN: 0019-9567
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: For most, if not all, organisms, iron (Fe) is an essential element. In response to the nutritional requirement for Fe, bacteria evolved complex systems to acquire the element from the environment, The genes encoding these systems are often coordinately regulated in response to the Fe concentration. Recent investigations revealed that Bordetella avium, a respiratory pathogen of birds, expressed a number of Fe-regulated genes (T. D. Connell, A. Dickenson, A. J. Martone, K. T. Militello, M. J. Filiatraut, M. L. Hayman, and J. Pitula, Infect. Immun. 66:3597-3605, 1998). By using manganese selection on an engineered strain of B. avium that carried an Fe-regulated alkaline phosphatase reporter gene, a mutant was obtained that was affected in expression of Fe-regulated genes. To determine if Fe-dependent regulation in B. avium was mediated by a %fur% -like %gene%, a fragment of the B. avium chromosome, corresponding to the fur locus of B, pertussis, was cloned by PCR. Sequencing revealed that the fragment from B. avium encoded a polypeptide with 92% identity to the Fur protein of B. pertussis. In vivo experiments showed that the cloned gene complemented H1780, a fur mutant of Escherichia coil. Southern hybridizations and PCRs demonstrated that the manganese mutant had a deletion of 2 to 3 Mbp of nucleotide sequence in the region located immediately 5' of the fur open reading frame. A spontaneous PCR-derived mutant of the R. avium %fur% %gene% was isolated that encoded a Fur protein in which a histidine was substituted for an arginine at amino acid position 18 (R18H). Genetic analysis showed that the R18H mutant gene when cloned into a low-copy-number vector did not complement the fur mutation in H1780, However, the R18H mutant gene was able to complement the fur mutation when cloned into a high-copy-number vector. The cloned wild-type %fur% %gene% will be useful as a genetic tool to identify Fur-regulated genes in the B. avium chromosome.

3/3,AB/5 (Item 3 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

09909571 References: 64
TITLE: Iron-responsive gene regulation in a Campylobacter jejuni fur mutant
AUTHOR(S): vanVliet AHM; Wooldridge KG; Ketley JM (REPRINT)
CORPORATE SOURCE: UNIV LEICESTER,DEPT GENET, UNIV RD/LEICESTER LE1 7RH/LEICS/ENGLAND/ (REPRINT); UNIV LEICESTER,DEPT GENET/LEICESTER LE1 7RH/LEICS/ENGLAND/
PUBLICATION TYPE: JOURNAL
PUBLICATION: JOURNAL OF BACTERIOLOGY, 1998, V180, N20 (OCT), P5291-5298
GENUINE ARTICLE#: 127JD

PUBLISHER: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW,
WASHINGTON, DC 20005-4171
ISSN: 0021-9193
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: The expression of iron-regulated systems in gram-negative bacteria is generally controlled by the Fur protein, which represses the transcription of iron-regulated promoters by using Fe2+ as a cofactor. Mutational analysis of the Campylobacter jejuni %fur% %gene% was carried out by generation of a set of mutant copies of fur which had a kanamycin or chloramphenicol resistance gene introduced into the regions encoding the N and C termini of the Fur protein. The mutated genes mere recombined into the C. jejuni NCTC 11168 chromosome, and putative mutants were confirmed by Southern hybridization. C. jejuni mutants were obtained only when the resistance genes were transcribed in the same orientation as the %fur% %gene%. The C. jejuni fur mutant grew slower than the parental strain. Comparison of protein profiles of fractionated C. jejuni cells grown in low- or high-iron medium indicated derepressed expression of three iron-regulated outer membrane proteins with molecular masses of 70, 75, and 80 kDa. Characterization by N-terminal amino acid sequencing showed the 75-kDa protein to be identical to CfrA, a Campylobacter coil siderophore receptor homologue, whereas the 70 kDa protein was identified as a new siderophore receptor homologue, Periplasmic fractions contained four derepressed proteins with molecular masses of 19, 29, 32, and 36 kDa, The 19-kDa protein has been previously identified, but its function is unknown. The cytoplasmic fraction contained two iron-repressed and two iron-induced proteins with molecular masses of 26, 55, 31, and 40 kDa, respectively. The two iron-repressed proteins have been previously identified as the oxidative stress defense proteins catalase (KatA) and alkyl hydroperoxide reductase (AhpC), AhpC and KatA were still iron regulated in the fur mutant, suggesting the presence of Fur-independent iron regulation. Further analysis of the C, jejuni iron and Fur regulons by using two-dimensional gel electrophoresis demonstrated the total number of iron- and Fur-regulated proteins to be loner than for other bacterial pathogens.

3/3,AB/6 (Item 4 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

05728818 References: 39
TITLE: IDENTIFICATION, CLONING, AND SEQUENCING OF A GENE REQUIRED FOR FERRIC VIBRIOBACTIN UTILIZATION BY VIBRIO CHOLERAE
AUTHOR(S): BUTTERTON JR; CALDERWOOD SB (Reprint)
CORPORATE SOURCE: MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114 (Reprint); MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114; HARVARD UNIV,SCH MED,DEPT MICROBIOL & MOLEC GENET/BOSTON//MA/02115
PUBLICATION: JOURNAL OF BACTERIOLOGY, 1994, V176, N18 (SEP), P5631-5638
GENUINE ARTICLE#: PF222
ISSN: 0021-9193
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: Chromosomal DNA downstream of the Vibrio cholerae ferric vibriobactin receptor gene, viuA, was cloned and sequenced, revealing an 813-bp open reading frame encoding a deduced protein of 271 amino acids. In vitro transcription-translation of this DNA confirmed expression of a protein of the expected size. A deletion mutation of this gene, viuB, was created in the classical V. cholerae strain O395 by in vivo marker exchange. By cross-feeding studies, this mutant was unable to utilize exogenous ferric vibriobactin but synthesized the siderophore normally; synthesis of siderophore by the mutant was also confirmed by the Arnow assay. Complementation of the mutant with a plasmid encoding only viuB restored ferric vibriobactin utilization to normal. Unexpectedly, hydropathicity analysis of ViuB did not reveal a signal sequence or transmembrane domain, suggesting that ViuB is not a periplasmic or membrane protein but may be a cytoplasmic protein involved in ferric vibriobactin uptake and processing, perhaps analogous to the Escherichia coli protein Fes. ViuB was not, however, homologous to Fes or to other proteins in the database. Complementation studies revealed that the cloned V. cholerae viuB

gene could complement an E. coli fes mutant but that the cloned E. coli fes gene could not complement a V. cholerae viuB mutant; Northern (RNA) blot analysis of RNA from wild-type V. cholerae grown in high- and low-iron media revealed a monocistronic viuB message that was negatively regulated by iron at the transcriptional level. The promoter of viuB was located by primer extension and contained a nucleotide sequence highly homologous to the E. coli Fur binding consensus sequence, suggesting that expression of viuB is under the control of the V. cholerae %fur% %gene%.

3/3,AB/7 (Item 5 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

05468121 References: 44
TITLE: CHARACTERIZATION OF THE VIBRIO CHOLERAE OUTER MEMBRANE HEME TRANSPORT PROTEIN HUTA - SEQUENCE OF THE GENE, REGULATION OF EXPRESSION, AND HOMOLOGY TO THE FAMILY OF TONB-DEPENDENT PROTEINS
AUTHOR(S): HENDERSON DP; PAYNE SM (Reprint)
CORPORATE SOURCE: UNIV TEXAS,DEPT MICROBIOL/AUSTIN//TX/78712 (Reprint); UNIV TEXAS,DEPT MICROBIOL/AUSTIN//TX/78712
PUBLICATION: JOURNAL OF BACTERIOLOGY, 1994, V176, N11 (JUN), P3269-3277
GENUINE ARTICLE#: NN851
ISSN: 0021-9193
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The regulation of hutA, the Vibrio cholerae gene encoding a 77-kDa iron-regulated outer membrane protein required for heme iron utilization, was characterized, and the DNA sequence of the gene was determined. A hutA::Tn5 lac fusion generated previously (D. P. Henderson and S. M. Payne, Mel. Microbiol. 7:461-469, 1993) was transformed into Fur(-) and Fur(+) strains of Escherichia coli and V. cholerae. The results of beta-galactosidase assays on the transformed strains demonstrated that transcription of hutA is regulated by the Fur repressor protein in E. coil and at least partially regulated by Fur in V. cholerae. Analysis of the DNA sequence of hutA indicated that a sequence homologous to the E. coli consensus Fur box was present in the promoter region of hutA. The amino acid sequence of HutA is homologous to those of several TonB-dependent outer member proteins. However, when the V. cholerae heme utilization system, which requires one or more genes encoded by the recombinant plasmid pHUT10 in addition to hutA Carried on a second vector, was transferred to a wild-type strain and an isogenic tonB mutant of E. coli, the tonB mutant could utilize heme iron as efficiently as the wild-type strain. These data indicate that the V. cholerae heme utilization system reconstituted in E. coli does not require a functional TonB protein. The tonB mutant transformed with the heme utilization plasmids could not utilize the siderophore ferrichrome as an iron source, indicating that none of the genes encoded on the heme utilization plasmids complements the tonB defect in E. coli. It is possible that a gene(s) encoded by the recombinant heme utilization plasmids encodes a protein serving a TonB-like function in V. cholerae. A region in the carboxy terminus of HutA is homologous to the horse hemoglobin zeta chain, and the amino acids involved in forming the heme pocket in the zeta chain are conserved in HutA. These data suggest that this region of HutA is involved in heme binding.

3/3,AB/8 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

05375535 Genuine Article#: VU635 Number of References: 43
Title: IDENTIFICATION AND PURIFICATION OF A HEMOGLOBIN-BINDING OUTER-MEMBRANE PROTEIN FROM NEISSERIA-GONORRHOEAE (Abstract Available)
Author(s): CHEN CJ; SPARLING PF; LEWIS LA; DYER DW; ELKINS C
Corporate Source: UNIV N CAROLINA,SCH MED,DEPT MED/CHAPEL HILL//NC/27599; UNIV N CAROLINA,SCH MED,DEPT MED/CHAPEL HILL//NC/27599; UNIV OKLAHOMA,HLTH SCI CTR,DEPT MICROBIOL & IMMUNOL/OKLAHOMA CITY//OK/73190
Journal: INFECTION AND IMMUNITY, 1996, V64, N12 (DEC), P5008-5014
ISSN: 0019-9567

Language: ENGLISH Document Type: ARTICLE
Abstract: The majority of in vitro-grown Neisseria gonorrhoeae strains were unable to use hemoglobin as the sole source of iron for growth (Hgb(-)), but a minor population was able to do so (Hgb(+)), The ability of Hgb(+) gonococci to utilize hemoglobin as the iron source was associated with the expression of an iron-repressible 89-kDa hemoglobin-binding protein in the outer membrane. The N-terminal amino acid sequence of this protein revealed amino acids, from positions 2 to 16, identical to those of HpuB, an 85 kDa iron-regulated hemoglobin-haptoglobin utilization outer membrane protein of %Neisseria% %meningitidis%, Isogenic mutants constructed by allelic replacement with a meningococcal hpu::mini-Tn3erm construct no longer expressed the 89-kDa protein. Mutants could not utilize hemoglobin to support growth but still grew on heme. Thus, the gonococcal HpuB homolog is a functional hemoglobin receptor and is essential for growth with hemoglobin.

3/3,AB/9 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

05165015 Genuine Article#: VE443 Number of References: 41
Title: OUTER-MEMBRANE PROTEIN B1, AN IRON-REPRESSIBLE PROTEIN CONSERVED IN THE OUTER-MEMBRANE OF MORAXELLA (BRANHAMELLA) CATARRHALIS, BINDS HUMAN TRANSFERRIN (Abstract Available)
Author(s): CAMPAGNARI AA; DUCEY TF; REBMANN CA
Corporate Source: SUNY BUFFALO,DIV INFECT DIS,DEPT MED,BIOMED RESBLDG,3435 BAILEY AVE/BUFFALO//NY/14214; SUNY BUFFALO,DEPT MICROBIOL/BUFFALO//NY/14214; SUNY BUFFALO,DEPT CLIN LAB SCI/BUFFALO//NY/14214
Journal: INFECTION AND IMMUNITY, 1996, V64, N9 (SEP), P3920-3924
ISSN: 0019-9567
Language: ENGLISH Document Type: ARTICLE
Abstract: Moraxella (Branhamella) catarrhalis is a gram-negative human mucosal pathogen, which primarily causes otitis media in young children. However, this bacterium is also a common cause of lower respiratory tract infections in adults with underlying lung disease. Our previous data have shown that M. catarrhalis expresses iron-repressible outer membrane proteins in response to iron Imitation. We have extended these observations to demonstrate that one of these proteins, termed outer membrane protein (OMP) B1, binds human transferrin. Using a newly developed monoclonal antibody to OMP B1, we determined that this protein is conserved in the iron-stressed outer membranes of all clinical isolates of M. catarrhalis tested to date. Furthermore, our data have confirmed that children infected with M. catarrhalis have immunoglobulin G antibodies to OMP B1 in their convalescent sera. These current data suggest that OMP B1 is immunogenic and expressed in vivo and may be involved in an iron uptake mechanism utilized by M. catarrhalis.

3/3,AB/10 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

05021840 Genuine Article#: UZ996 Number of References: 54
Title: UTILIZATION OF HEMIN AND HEMOGLOBIN BY VIBRIO-VULNIFICUS BIOTYPE-2 (Abstract Available)
Author(s): FOUZ B; MAZOY R; LEMOS ML; DELOLMO MJ; AMARO C
Corporate Source: UNIV VALENCIA,DEPT MICROBIOL,FAC BIOL,AVDA DR MOLINER 50/E-46100 BURJASSOT/VALENCIA/SPAIN/; UNIV VALENCIA,DEPT MICROBIOL,FAC BIOL/E-46100 BURJASSOT/VALENCIA/SPAIN/; UNIV SANTIAGO DE COMPOSTELA,DEPT MICROBIOL & PARASITOL,FAC CIENCIAS/E-27002 LUGO//SPAIN/
Journal: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, 1996, V62, N8 (AUG), P 2806-2810
ISSN: 0099-2240
Language: ENGLISH Document Type: ARTICLE
Abstract: The eel pathogen Vibrio vulnificus biotype 2 is able to use

hemoglobin (Hb) and hemin (Hm) to reverse iron limitation. In this study, the adjuvant effect of both compounds on eel pathogenicity has been evaluated and confirmed, Further, we have studied the heme-iron acquisition mechanism displayed by this bacterium. Whole cells were capable of binding Hb and Hm, independently of (i) iron levels in growth medium and (ii) the presence of polysaccharide capsules on bacterial surface. The Hb- and Hm-binding capacity was retained by the outer membrane protein (OMP) fraction and was abolished after proteolytic digestion of OMP samples, Western blotting (immunoblotting) of denatured OMPs revealed hat two major protein bands of 36 and 32 kDa were involved in both Km and Hb binding, The expression of these proteins was not affected by iron levels. In addition, V. vulnificus biotype 2 produced extracellular proteases, not regulated by iron, that were active against native Hb. In conclusion, the overall data suggest that the eel pathogen V. vulnificus biotype 2 can obtain iron by means of a mechanism which involves a direct interaction between the heme moiety and constitutive OMPs.

3/3,AB/11 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

05011765 Genuine Article#: UZ047 Number of References: 51
Title: HMBR OUTER-MEMBRANE RECEPTORS OF PATHOGENIC NEISSERIA SPP - IRON-REGULATED, HEMOGLOBIN-BINDING PROTEINS WITH A HIGH-LEVEL OF PRIMARY STRUCTURE CONSERVATION (Abstract Available)
Author(s): STOJILJKOVIC I; LARSON J; HWA V; ANIC S; SO M
Corporate Source: OREGON HLTH SCI UNIV,DEPT MOLEC MICROBIOL & IMMUNOL/PORTLAND//OR/97201; EMORY UNIV,DEPT MICROBIOL & IMMUNOL/ATLANTA//GA/30322
Journal: JOURNAL OF BACTERIOLOGY, 1996, V178, N15 (AUG), P4670-4678
ISSN: 0021-9193
Language: ENGLISH Document Type: ARTICLE
Abstract: We have recently cloned and characterized the hemoglobin receptor gene from %Neisseria% %meningitidis% serogroup C. N. meningitidis tells expressing HmbR protein were able to bind biotinylated hemoglobin, and the binding was specifically inhibited by unlabeled hemoglobin and not heme. The HmbR-mediated hemoglobin binding activity of N. meningitidis cells was shown to be iron regulated, The presence of hemoglobin but not heme in the growth medium stimulated HmbR-mediated hemoglobin binding activity. The efficiency of utilization of different hemoglobins by the HmbR-expressing N. meningitidis cells was shown to be species specific; human hemoglobin was the best source of iron, followed by horse, rat, turkey, dog, mouse, and sheep hemoglobins. The phenotypic characterization of HmbR mutants of some clinical strains of N. meningitidis suggested the existence of two unrelated hemoglobin receptors. The HmbR-unrelated hemoglobin receptor was shown to be identical to Hpu, the hemoglobin-haptoglobin receptor of N. meningitidis. The Hpu-dependent hemoglobin utilization system was not able to distinguish between different sources of hemoglobin; all animal hemoglobins were utilized equally well. HmbR-like genes are also present in N. meningitidis serogroups A and B, Neisseria gonorrhoeae MS11 and FA19, Neisseria perflava, and Neisseria polysaccharea. The hemoglobin receptor genes from N. meningitidis serogroups A and B and N. gonorrhoeae MS11 were cloned, and their nucleotide sequences were determined, The nucleotide sequence identity ranged between 86.5% (for N. meningitidis serogroup B hmbR and MS11 hmbR) and 93.4% (for N. meningitidis serogroup B hmbR and N. meningitidis serogroup C hmbR). The deduced amino acid sequences of these neisserial hemoglobin receptors were also highly related, with overall 84.7% conserved amino acid residues. A stop codon was found in the hmbR gene of N. gonorrhoeae MS11. This strain was still able to use hemoglobin and hemoglobin-haptoglobin complexes as iron sources, indicating that some gonococci may express only the HmbR-independent hemoglobin utilization system.

3/3,AB/12 (Item 5 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

04980181 Genuine Article#: UW876 Number of References: 14
Title: ONE-STEP METAL-AFFINITY METHOD FOR THE PURIFICATION OF THE IRON-BINDING PROTEIN FBP OF %NEISSERIA%-%MENINGITIDIS% (Abstract Available)
Author(s): FERRON L; PINTOR M; GOMEZ JA; CRIADO MT; FERREIROS C
Corporate Source: UNIV SANTIAGO DE COMPOSTELA,FAC FARM,DEPT MICROBIOL & PARASITOL/SANTIAGO COMPOSTE//SPAIN/; UNIV SANTIAGO DE COMPOSTELA,FAC FARM,DEPT MICROBIOL & PARASITOL/SANTIAGO COMPOSTE//SPAIN/
Journal: JOURNAL OF MICROBIOLOGICAL METHODS, 1996, V25, N3 (JUN), P233-236
ISSN: 0167-7012
Language: ENGLISH Document Type: ARTICLE
Abstract: A one-step method for the purification of the iron-binding protein, Fbp, from %Neisseria% %meningitidis% has been developed using affinity chromatography on iron-Sepharose. This method allowed the purification of the protein in non-denaturing conditions and in a similar way to those used previously. Our results demonstrate the homogeneity of the purified protein as tested by SDS-PAGE and IEF.

3/3,AB/13 (Item 6 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

04839868 Genuine Article#: UL527 Number of References: 68
Title: ACQUISITION OF IRON BY THE NON-SIDEROPHORE-PRODUCING PSEUDOMONAS-FRAGI (Abstract Available)
Author(s): CHAMPOMIERVERGES MC; STINTZI A; MEYER JM
Corporate Source: UNIV STRASBOURG 1,CNRS,URA D1481,LAB MICROBIOL & GENET,28 RUE GOETHE/F-67083 STRASBOURG//FRANCE/; UNIV STRASBOURG 1,CNRS,URA D1481,LAB MICROBIOL & GENET/F-67083 STRASBOURG//FRANCE/; INRA,LAB RECH VIANDE/F-78352 JOUY EN JOSAS//FRANCE/
Journal: MICROBIOLOGY-UK, 1996, V142, MAY (MAY), P1191-1199
ISSN: 1350-0872
Language: ENGLISH Document Type: ARTICLE
Abstract: The iron requirement, siderophore production and iron uptake mechanism of the type strain Pseudomonas fragi ATCC 4973 and five P. fragi isolates from meat were analysed. The strains exhibited a high sensitivity to iron starvation: their growth was strongly inhibited in medium supplemented with the iron chelator ethylenediamine di(hydroxyphenylacetic acid) or in medium treated with 8-hydroxyguinoline to remove contaminating iron. No siderophores were detectable in the growth supernatants of iron-starved cells. Cross-feeding experiments in iron-depleted medium showed, however, that the bacterial growth could be strongly stimulated by siderophores of foreign origin including desferriferrioxamine B, enterobactin and some pyoverdines. Moreover, all the strains were capable of efficiently using the iron sources present in their natural environment, i.e. transferrin, lactoferrin and haemoglobin. Iron starvation led to the specific production of supplementary outer-membrane proteins of apparent molecular mass ranging from 80 to 88 kDa. Furthermore, growth in the presence of exogenous siderophores resulted, in some strains, in the induction of siderophore-mediated iron uptake systems. For one strain the concomitant synthesis of an iron-regulated, siderophore-inducible outer-membrane protein was observed.

3/3,AB/14 (Item 7 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

04635265 Genuine Article#: TY365 Number of References: 48
Title: SIDEROPHORE-MEDIATED IRON ACQUISITION MECHANISMS IN VIBRIO-VULNIFICUS BIOTYPE-2 (Abstract Available)
Author(s): BIOSCA EG; FOUZ B; ALCAIDE E; AMARO C
Corporate Source: UNIV VALENCIA,FAC BIOL,DEPT MICROBIOL & ECOL,AVDA DR MOLINER 50/E-46100 VALENCIA//SPAIN/; UNIV VALENCIA,FAC BIOL,DEPT

MICROBIOL & ECOL/E-46100 VALENCIA//SPAIN/
Journal: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, 1996, V62, N3 (MAR), P 928-935
ISSN: 0099-2240
Language: ENGLISH Document Type: ARTICLE
Abstract: Vibrio vulnificus biotype 2 is a primary pathogen for eels and, as has recently been suggested, an opportunistic pathogen for humans. In this study we have investigated the ability of V. vulnificus biotype 2 to obtain iron by siderophore-mediated mechanisms and evaluated the importance of free iron in vibriosis. The virulence degree for eels was dependent on iron availability from host fluids, as was revealed by a reduction in the 50% lethal dose for iron-overloaded eels. This biotype produced both phenolate- and hydroxamate-type siderophores of an unknown nature and two new outer membrane proteins of around 84 and 72 kDa in response to iron starvation. No alterations in lipopolysaccharide patterns were detected in response to iron stress, Finally, our data suggest that V. vulnificus biotype 2 uses the hydroxamate-type siderophore for removal of iron from transferrin rather than relying on a receptor for this iron-binding protein.

3/3,AB/15 (Item 8 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01920368 Genuine Article#: JL957 Number of References: 60
Title: FUR REGULATION IN YERSINIA SPECIES (Abstract Available)
Author(s): STAGGS TM; PERRY RD
Corporate Source: UNIV KENTUCKY,DEPT MICROBIOL & IMMUNOL,MS415 CHANDLER MED CTR/LEXINGTON//KY/40536; UNIV KENTUCKY,DEPT MICROBIOL & IMMUNOL,MS415 CHANDLER MED CTR/LEXINGTON//KY/40536
Journal: MOLECULAR MICROBIOLOGY, 1992, V6, N17 (SEP), P2507-2516
ISSN: 0950-382X
Language: ENGLISH Document Type: ARTICLE
Abstract: The effects of iron have been linked with several phenomena including regulation of membrane proteins; however, the mechanism of iron regulation is not well characterized in Yersinia pestis. It is well known that in Escherichia coli, the %fur% %gene% product mediates negative transcriptional regulation of several genes in response to iron. We have cloned a Y. pestis %fur% %gene% which is highly homologous to the E. coli %fur% regulatory %gene%. The sequence of the Y. pestis %fur% %gene% exhibits 75% homology to the E. coli gene at the nucleotide level, and 84% homology at the predicted amino acid level. The Y. pestis %fur% %gene% is transcribed as a single gene message of approximately 0.5 kb which encodes an approximately 16 kDa protein when expressed in E. coli minicells. A Yersinia enterocolitica fur mutant exhibits hypersensitivity to the Y. pestis bacteriocin, pesticin; the cloned Y. pestis %fur% %gene% restores wild-type levels of pesticin sensitivity. Furthermore, iron regulation of at least five surface proteins in this Y. enterocolitica fur mutant is restored by transcomplementation with the Y. pestis %fur% %gene%. These data indicate that Y. pestis and Y. enterocolitica possess homologous Fur systems which regulate expression of proteins in response to iron availability.

3/3,AB/16 (Item 9 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01740384 Genuine Article#: HX278 Number of References: 46
Title: CLONING, SEQUENCING, AND TRANSCRIPTIONAL REGULATION OF VIUA, THE GENE ENCODING THE FERRIC VIBRIOBACTIN RECEPTOR OF VIBRIO-CHOLERAE (Abstract Available)
Author(s): BUTTERTON JR; STOEBNER JA; PAYNE SM; CALDERWOOD SB
Corporate Source: MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114; MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114; UNIV TEXAS,DEPT MICROBIOL/AUSTIN//TX/78712; HARVARD UNIV,SCH MED,DEPT MICROBIOL & GENET/BOSTON//MA/02115

Journal: JOURNAL OF BACTERIOLOGY, 1992, V174, N11 (JUN), P3729-3738
Language: ENGLISH Document Type: ARTICLE
Abstract: A 74-kDa iron-regulated outer membrane protein of Vibrio cholerae acts as the receptor for the V. cholerae iron-siderophore complex, ferric vibriobactin. MBG14, a mutant of V. cholerae 0395 containing a TnphoA insertion in a gene designated viuA, lacks this 74-kDa outer membrane protein and is unable to bind or utilize exogenous ferric vibriobactin. Introduction of a plasmid containing the complete viuA coding sequence and 513 bp of upstream DNA into MBG14 restored ferric vibriobactin utilization to the mutant. The DNA insert in this plasmid was sequenced, revealing a single open reading frame of 2,061 bp, encoding a deduced protein of 687 amino acids with a predicted molecular mass of 76,417 Da and a predicted initial signal sequence of 37 amino acids. ViuA showed only weak homology to two iron-regulated outer membrane proteins in Escherichia coli, IutA and FecA. Construction of viuA::TnphoA gene fusions allowed study of the regulation of viuA expression by iron. This regulation in E. coli was dependent on the %fur% %gene%. Northern (RNA) blot analysis of RNA from wild-type V. cholerae grown in high- and low-iron media revealed a monocistronic viuA message that was negatively regulated by iron at the transcriptional level. Primer extension analysis identified a single transcriptional start site, located 243 bp above the translational start site. The promoter region of viuA contained two interrupted dyad symmetric nucleotide sequences, overlapping the -10 and -35 boxes, each similar to the E. coli Fur binding consensus sequence. Another iron-regulated gene in V. cholerae that is negatively regulated by fur, irgA, requires a positive transcriptional activator (irgB) for expression. However, a strain of V. cholerae mutant in irgB was unaffected in viuA expression. These studies suggest that there is conserved, global coordinate iron regulation in V. cholerae by fur; additional regulatory factors, superimposed upon the fur system, may provide more precise control of individual iron-regulated genes.

3/3,AB/17 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

139241254 CA: 139(16)241254e JOURNAL
Identification of iron-activated and -repressed Fur-dependent genes by transcriptome analysis of Neisseria meningitidis group B
AUTHOR(S): Grifantini, Renata; Sebastian, Shite; Frigimelica, Elisabetta; Draghi, Monia; Bartolini, Erika; Muzzi, Alessandro; Rappuoli, Rino; Grandi, Guido; Genco, Caroline Attardo
LOCATION: Chiron SpA, Siena, Italy
JOURNAL: Proc. Natl. Acad. Sci. U. S. A. (Proceedings of the National Academy of Sciences of the United States of America) DATE: 2003 VOLUME: 100 NUMBER: 16 PAGES: 9542-9547 CODEN: PNASA6 ISSN: 0027-8424
LANGUAGE: English PUBLISHER: National Academy of Sciences

3/3,AB/18 (Item 2 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

130071518 CA: 130(6)71518p PATENT
Live attenuated bacterial vaccines containing a modified iron uptake fur gene
INVENTOR(AUTHOR): Baldwin, Thomas John; Borriello, Saverio Peter; Palmer, Helen Mary
LOCATION: UK,
ASSIGNEE: Medical Research Council
PATENT: PCT International ; WO 9856901 A2 DATE: 19981217
APPLICATION: WO 98GB1683 (19980609) *GB 9711964 (19970609)
PAGES: 49 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12N-015/00A
DESIGNATED COUNTRIES: AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN; CU; CZ; DE; DK; EE; ES; FI; GB; GE; GH; GM; GW; HU; ID; IL; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; UA; UG; US; UZ; VN; YU;

applicant

ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS ; MW; SD; SZ; UG; ZW; AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; ML; MR; NE; SN; TD; TG

3/3,AB/19 (Item 1 from file: 654)
DIALOG(R)File 654:US Pat.Full.

0005335587
Derwent Accession: 2003-787326
Compositions and methods for treatment of neoplastic disease
Inventor: David Terman, INV
Correspondence Address: David S. Terman, P.O. Box 987, Pebble beach, CA, 93953, US

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 20030157113	A1	20030821	US 2000751708	20001228
Provisional				US 60-173371	19991228

Fulltext Word Count: 151651

Abstract:
The present invention comprises compositions and methods for treating a tumor or neoplastic disease in a host, The methods employ conjugates comprising superantigen polypeptides, nucleic acids with other structures that preferentially bind to tumor cells and are capable of inducing apoptosis. Also provided are superantigen-glycolipid conjugates and vesicles that are loaded onto antigen presenting cells to activate both T cells and NKT cells. Cell-based vaccines comprise tumor cells engineered to express a superantigen along with glycolipids products which, when expressed, render the cells capable of eliciting an effective anti-tumor immune response in a mammal into which these cells are introduced. Included among these compositions are tumor cells, hybrid cells of tumor cells and accessory cells, preferably dendritic cells. Also provided are tumoricidal T cells and NKT cells devoid of inhibitory receptors or inhibitory signaling motifs which are hyperresponsive to the the above compositions and lipid-based tumor associated antigens that can be administered for adoptive immunotherapy of cancer and infectious diseases.

3/3,AB/20 (Item 2 from file: 654)
DIALOG(R)File 654:US Pat.Full.

0005329374
Derwent Accession: 2003-897737
Staphylococcus aureus genes and polypeptides
Inventor: Andrew Simpson, INV
Gil Choi, INV
Assignee: Human Genome Sciences, Inc. (03), Rockville, MD, 20850, US, 9410 Key West Avenue
Correspondence Address: HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 20030153733	A1	20030814	US 2002278946	20021024
Division	US 6521441			US 2002830217	20020115
A371	PENDING			WO 99US6199	19990318
Provisional				US 60-78862	19980320
Provisional				US 60-80296	19980401

Provisional US 60-84674 19980507

Fulltext Word Count: 34439

Abstract:
The present invention relates to 11 novel genes from S. aureus and the polypeptides they encode. Also provided as are vectors, host cells, antibodies and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of S. aureus polypeptide activity. The invention additionally relates to diagnostic methods for detecting Staphylococcus nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by Staphylococcus.

3/3,AB/21 (Item 3 from file: 654)
DIALOG(R)File 654:US Pat.Full.

0005126116
Derwent Accession: 2003-361759
Compositions and methods for treatment of neoplastic disease
Inventor: David Terman, INV
Correspondence Address: David S. Terman, P.O. Box 987, Pebble Beach, CA, 93953, US

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 20020177551	A1	20021128	US 2001870759	20010530
Provisional				US 60-208128	20000531

Fulltext Word Count: 164990

Abstract:
The present invention comprises compositions and methods for treating a tumor or neoplastic disease in a host, The methods employ conjugates comprising superantigen polypeptides, nucleic acids with other structures that preferentially bind to tumor cells and are capable of inducing apoptosis. Also provided are superantigen-glycolipid conjugates and vesicles that are loaded onto antigen presenting cells to activate both T cells and NKT cells. Cell-based vaccines comprise tumor cells engineered to express a superantigen along with glycolipids products which, when expressed, render the cells capable of eliciting an effective anti-tumor immune response in a mammal into which these cells are introduced. Included among these compositions are tumor cells, hybrid cells of tumor cells and accessory cells, preferably dendritic cells. Also provided are tumoricidal T cells and NKT cells devoid of inhitory receptors or inhibitory signaling motifs which are hyperresponsive to the the above compositions and lipid-based tumor associated antigens that can be administered for adoptive immunotherapy of cancer and infectious diseases.

3/3,AB/22 (Item 4 from file: 654)
DIALOG(R)File 654:US Pat.Full.

0004920283
Derwent Accession: 2001-398123
Antigen preparations
Inventor: Thomas Baldwin, INV
Paul Williams, INV

Simon Swift, INV
Cornelia McLean, INV
Christopher Holmes, INV
Correspondence Address: KLARQUIST SPARKMAN CAMPBELL LEIGH & WHINSTON, LLP Suite 1600, One World Trade Center 121 S.W. Salmon Street, Portland , OR, 97204-2988, US

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 20010031268	A1	20011018	US 2000740048	20001218
Provisional				US 60-172485	19991217

Fulltext Word Count: 7244

Abstract:
Bacterial antigen preparations for use as live or killed immunogens and vaccines can be produced by culture of bacteria such as Neisseria in medium comprising norepinephrine or other catechol-group-containing growth inducer of bacterial growth, harvesting and pharmaceutical formulation. The antigen preparations can comprise bacterial protein(s) inducible by norepinephrine.

3/3,AB/23 (Item 5 from file: 654)
DIALOG(R)File 654:US Pat.Full.

4826849
Derwent Accession: 1999-580304
Utility
C/ Staphylococcus aureus genes and polypeptides
Inventor: Simpson, Andrew J. G., Sao Paulo, BR
Choi, Gil H., Rockville, MD
Assignee: Human Genome Sciences, Inc. (02), Rockville, MD
Ludwig Institute For Cancer Research (03), Sao Paulo, BR
Human Genome Sciences Inc
Ludwig Institite for Cancer Research BR
Ludwig Inst For Cancer Res BR (Code: 38350 64358)
Examiner: Navarro, Mark (Art Unit: 165)
Law Firm: Human Genome Sciences, Inc.

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 6521441	A	20030218	US 2002830217	20020115
PCT	WO 9947662		19990923	WO 99US6199	19990318
		371:			
		102e:			

Fulltext Word Count: 32270

Abstract:
The present invention relates to 11 novel genes from S. aureus and the polypeptides they encode. Also provided are vectors, host cells, antibodies and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of S. aureus polypeptide activity. The invention additionally relates to diagnostic methods for detecting Staphylococcus nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by Staphylococcus.

3/3,AB/24 (Item 6 from file: 654)
DIALOG(R)File 654:US Pat.Full.

4180640
Derwent Accession: 1999-468143
Utility
CERTIFICATE OF CORRECTION
C/ Method and materials for detecting Legionella pneumophila
Inventor: Cianciotto, Nicholas P., Evanston, IL
Hickey, Erin K., Evanston, IL
Assignee: Northwestern University (02), Evanston, IL
Northwestern University (Code: 60920)
Examiner: Myers, Carla J. (Art Unit: 164)
Law Firm: Sheridan Ross P.C.

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 5935782	A	19990810	US 96766858	19961213
Provisional				US 60-11545	19960213

Fulltext Word Count: 15861
Abstract:
The invention provides novel genes and proteins of Legionela pneumophila. The invention also provides methods of detecting or quantitating L. pneumophila using these genes, mRNAs encoded by the genes, or proteins encoded by the genes as targets. Nucleic acids designed to hybridize with the genes or mRNAs encoded by the genes, or antibodies that bind specifically to the proteins, are used in the methods, and the nucleic acids and antibodies can be provided in kits.

3/3,AB/25 (Item 1 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE

00040756 94088062
Cloning and sequence analysis of the %fur% %gene% encoding an iron-regulatory protein of %Neisseria% %meningitidis%
Karhoff-Schweizer R.R.; Schryvers A.B.; Schweizer H.P.
ADDRESS: R.R. Karhoff-Schweizer, Canada
Journal: Gene, 141/1 (139-140), 1994
PUBLICATION DATE: 19940000
CODEN: GENED
ISSN: 0378-1119
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English

3/3,AB/26 (Item 1 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT

01021406
HUMAN GENES AND GENE EXPRESSION PRODUCTS ISOLATED FROM HUMAN PROSTATE
GENES HUMAINS ET PRODUITS D'EXPRESSION GENIQUES ISOLES D'UNE PROSTATE HUMAINE
Patent Applicant/Assignee:
CHIRON CORPORATION, 4560 Horton Street - R440, Emeryville, CA 94608, US, US (Residence), US (Nationality), (For all designated states except: US)
HYSEQ INC, 675 Almanor Avenue, Sunnyvale, CA 94086, US, US (Residence), US (Nationality), (For all designated states except: US)
Patent Applicant/Inventor:
ESCOBEDO Jaime, 1470 Lavorna Road, Alamo, CA 94507, US, US (Residence), CL (Nationality), (Designated only for: US)
GARCIA Pablo Dominguez, 882 Chenery Street, San Francisco, CA 94131, US, US (Residence), CL (Nationality), (Designated only for: US)
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US (Nationality), (Designated only for: US)
LAMSON George, 232 Sandringham Drive, Moraga, CA 94556, US, US (Residence), US (Nationality), (Designated only for: US)
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DICKSON Mark, 1411 Gabilan Drive, #B, Hollister, CA 95025, US, US (Residence), US (Nationality), (Designated only for: US)
DRMANAC Snezana, 850 East Greenwich Place, Palo Alto, CA 94303, US, US (Residence), YU (Nationality), (Designated only for: US)
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LESHKOWITZ Dena, 1 Mevo Brosh, 56452 Yehud, IL, IL (Residence), US (Nationality), (Designated only for: US)
KITA David, 899 Bounty Drive, Foster City, CA 94404, US, US (Residence), US (Nationality), (Designated only for: US)
GARCIA Veronica, 396 Ano Nuevo, Apt. 412, Sunnyvale, CA 94086, US, US (Residence), ES (Nationality), (Designated only for: US)
JONES Lee William, 396 Ano Nuevo #412, Sunnyvale, CA 94086, US, US (Residence), US (Nationality), (Designated only for: US)
STACHE-CRAIN Birgit, 345 South Mary Avenue, Sunnyvale, CA 94086, US, US (Residence), DE (Nationality), (Designated only for: US)
SCOTT Elizabeth M, 1267 Nash Street, Sonoma, CA 95476, US, US (Residence), US (Nationality), (Designated only for: US)

Legal Representative:
BLACKBURN Robert P (agent), Chiron Corporation, P.O. Box 8097, Emeryville, CA 94662-8097 (et al), US,

Patent and Priority Information (Country, Number, Date):
Patent: WO 200350236 A2 20030619 (WO 0350236)
Application: WO 2002US28214 20020904 (PCT/WO US0228214)
Priority Application: US 200112697 20011207

Designated States: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW
(EP) AT BE BG CH CY CZ DE DK EE ES FI FR GB GR IE IT LU MC NL PT SE SK TR
(OA) BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG
(AP) GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW
(EA) AM AZ BY KG KZ MD RU TJ TM

Publication Language: English
Filing Language: English
Fulltext Word Count: 86998

English Abstract

This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostics and therapeutics comprising such novel human polynucleotides, their corresponding genes or gene products, including probes, antisense nucleotides, and antibodies. The polynucleotides of the invention correspond to a polynucleotide comprising the sequence information of at least one of SEQ ID NOS:1-1477. The polypeptides of the invention correspond to a polypeptide comprising the amino acid sequence information of at least one of SEQ ID NOS:1478-1568.

French Abstract

L'invention se rapporte a de nouveaux polynucleotides humains et a leurs variantes, a leurs polypeptides codes et a leurs variantes, aux genes correspondant a ces polynucleotides et aux proteines exprimees par les genes. L'invention se rapporte egalement a des diagnostics et des therapies comprenant lesdits nouveaux polynucleotides humains, leurs genes correspondants ou leurs produits genetiques, y compris les sondes, les nucleotides antisens et les anticorps. Les polynucleotides de cette invention correspondent a un polynucleotide comprenant l'information de sequence d'au moins une des SEQ ID NOS:1-1477. Les polypeptides de cette invention correspondent, quant a eux, a un polypeptide comprenant l'information d'une sequence d'acides amines d'au moins une des SEQ ID

NOS:1478-1568.

3/3,AB/27 (Item 2 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT

00922886
HUMAN GENES AND GENE EXPRESSION PRODUCTS ISOLATED FROM HUMAN PROSTATE
GENES HUMAINS ET PRODUITS D'EXPRESSION GENETIQUE ISOLES DE LA PROSTATE HUMAINE

Patent Applicant/Assignee:
CHIRON CORPORATION, 4560 Horton Street, R440, Emeryville, CA 94608, US, US (Residence), US (Nationality), (For all designated states except: US)
HYSEQ INC, 675 Almanor Avenue, Sunnyvale, CA 94086, US, US (Residence), US (Nationality), (For all designated states except: US)
Patent Applicant/Inventor:
ESCOBEDO Jaime, 1470 Lavorna Road, Alamo, CA 94507, US, US (Residence), CL (Nationality), (Designated only for: US)
GARCIA Pablo Dominguez, 882 Chenery Street, San Francisco, CA 94131, US, US (Residence), CL (Nationality), (Designated only for: US)
KASSAM Altaf, 3810 Midvale Avenue, Oakland, CA 94602, US, US (Residence), US (Nationality), (Designated only for: US)
LAMSON George, 232 Sandringham Drive, Moraga, CA 94556, US, US (Residence), US (Nationality), (Designated only for: US)
DRMANAC Radoje, 850 East Greenwich Place, Palo Alto, CA 94303, US, US (Residence), US (Nationality), (Designated only for: US)
CRKVENJAKOV Radomir, 762 Haverhill Drive, Sunnyvale, CA 94068, US, US (Residence), YU (Nationality), (Designated only for: US)
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LABAT Ivan, 1006 Asbury Way, Mountain View, CA 94043, US, US (Residence), YU (Nationality), (Designated only for: US)
LESHKOWITZ Dena, 1 Mevo Brosh, Yehud, 56452, IL, IL (Residence), US (Nationality), (Designated only for: US)
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JONES William Lee, 396 Ano Nuevo #412, Sunnyvale, CA 94086, US, US (Residence), US (Nationality), (Designated only for: US)
STACHE-CRAIN Birgit, 345 South Mary Avenue, Sunnyvale, CA 94086, US, US (Residence), DE (Nationality), (Designated only for: US)
SCOTT Elizabeth M, 1267 Nash Street, Sonoma, CA 95476, US, US (Residence), US (Nationality), (Designated only for: US)
Legal Representative:
BOZICEVIC Karl (agent), Bozicevic, Field & Francis LLP, Suite 200, 200 Middlefield Road, Menlo Park, CA 94025, US,

Patent and Priority Information (Country, Number, Date):
Patent: WO 200255700 A2-A3 20020718 (WO 0255700)
Application: WO 2001US47349 20011207 (PCT/WO US0147349)
Priority Application: US 2000254648 20001207; US 2001275688 20010313
Designated States: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZM ZW
(EP) AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR
(OA) BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG
(AP) GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW
(EA) AM AZ BY KG KZ MD RU TJ TM
Publication Language: English
Filing Language: English
Fulltext Word Count: 87496

English Abstract
This invention relates to novel human polynucleotides and variants

thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostics and therapeutics comprising such novel human polynucleotides, their corresponding genes or gene products, including probes, antisense nucleotides, and antibodies. The polynucleotides of the invention correspond to a polynucleotide comprising the sequence information of at least one of SEQ ID NOS:1-1477. The polypeptides of the invention correspond to a polypeptide comprising the amino acid sequence information of at least one of SEQ ID NOS:1478-1568.

French Abstract
L'invention concerne de nouveaux polynucleotides humains et des variants de ceux-ci, leurs polypeptides codes et les variants de ceux-ci, des genes correspondant a ces polynucleotides et des proteines exprimees par ces genes. L'invention concerne egalement des diagnostics et therapies utilisant ces nouveaux polynucleotides humains, leurs genes correspondants ou leurs produits genetiques, y compris des sondes, des nucleotides antisens et des anticorps. Les polynucleotides decrits par la presente invention correspondent a un polynucleotide contenant les informations de sequence d'au moins une des SEQ ID NOS:1-1477. Les polypeptides decrits par la presente invention correspondent a un polypeptide comprenant des informations de sequence aminoacide d'au moins une des sequences SEQ ID NOS:1478-1568.

3/3,AB/28 (Item 3 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT

00812075
ANTIGEN PREPARATIONS
PREPARATIONS D'ANTIGENES
Patent Applicant/Assignee:
CANTAB PHARMACEUTICALS RESEARCH LIMITED, 310 Cambridge Science Park, Milton Road, Cambridge, Cambridgeshire CB4 0WG, GB, GB (Residence), GB (Nationality), (For all designated states except: US)
UNIVERSITY OF NOTTINGHAM, University Park, Nottingham, Nottinghamshire NG7 2RD, GB, GB (Residence), GB (Nationality), (For all designated states except: US)
Patent Applicant/Inventor:
BALDWIN Thomas John, 65 Trent Boulevard, Lady Bay, Westbridgeford, Nottingham, Nottinghamshire NG2 5BE, GB, GB (Residence), GB (Nationality), (Designated only for: US)
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Legal Representative:
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Patent and Priority Information (Country, Number, Date):
Patent: WO 200144278 A2-A3 20010621 (WO 0144278)
Application: WO 2000GB4874 20001218 (PCT/WO GB0004874)
Priority Application: GB 9929923 19991217
Designated States: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
(EP) AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR
(OA) BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG
(AP) GH GM KE LS MW MZ SD SL SZ TZ UG ZW
(EA) AM AZ BY KG KZ MD RU TJ TM
Publication Language: English

Filing Language: English
Fulltext Word Count: 6587

English Abstract
Bacterial antigen preparations for use as live or killed immunogens and vaccines can be produced by culture of bacteria such as Neisseria in medium comprising norepinephrine or other catechol-group-containing growth inducer of bacterial growth, harvesting and pharmaceutical formulation. The antigen preparations can comprise bacterial protein(s) inducible by norepinephrine.

French Abstract
Cette invention se rapporte a des preparations d'antigenes bacteriens destines a servir d'immunogenes et de vaccins vivants ou tues, qui peuvent etre produites par culture de bacteries telles que Neisseria, dans un milieu comprenant de la norepinephrine ou tout autre inducteur de croissance bacterienne contenant un groupe catechol, par recolte et par formulation pharmaceutique. Ces preparations d'antigene peuvent contenir une/des proteine(s) bacterienne(s) induisible(s) par la norepinephrine.

3/3,AB/29 (Item 4 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT

00749502
NOVEL ESSENTIAL BACTERIAL GENES AND THEIR PROTEINS
GENES BACTERIENS ESSENTIELS ET LEURS PROTEINES
NEUE ESSENTIELLE BAKTERIELLE GENE UND IHRE PROTEINE
Patent Applicant/Assignee:
BAYER AKTIENGESELLSCHAFT, D-51368 Leverkusen, DE, DE (Residence), DE (Nationality), (For all designated states except: US)
Patent Applicant/Inventor:
BROTZ Heike, Claudiusweg 9, D-42115 Wuppertal, DE, DE (Residence), DE (Nationality), (Designated only for: US)
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FREIBERG Christoph, Nullerstrasse 85, D-42115 Wuppertal, DE, DE (Residence), DE (Nationality), (Designated only for: US)
SPALTMANN Frank, 1008 Massachusetts Avenue, Apt. #403, Cambridge, MA 02138, US, US (Residence), DE (Nationality), (Designated only for: US)
WIELAND Bernd, Unterkirchen 38, D-42349 Wuppertal, DE, DE (Residence), DE (Nationality), (Designated only for: US)
LABISCHINSKI Harald, Katernberger Schulweg 80, D-42113 Wuppertal, DE, DE (Residence), DE (Nationality), (Designated only for: US)
Legal Representative:
BAYER AKTIENGESELLSCHAFT, D-51368 Leverkusen, DE
Patent and Priority Information (Country, Number, Date):
Patent: WO 200061792 A1 20001019 (WO 0061792)
Application: WO 2000EP2713 20000328 (PCT/WO EP0002713)
Priority Application: DE 19916176 19990410
Designated States: AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
(EP) AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
(OA) BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG
(AP) GH GM KE LS MW SD SL SZ TZ UG ZW
(EA) AM AZ BY KG KZ MD RU TJ TM
Publication Language: German
Filing Language: German
Fulltext Word Count: 14072

English Abstract
The invention relates to nucleic acids and to protein sequences derived from said nucleic acids which possess functions that are essential to the survival of Escherichia coli. The invention also relates to vectors and host cells that have been transformed with these vectors for expressing essential proteins of the type described above and to proteins produced

with these vectors. Finally, the invention also relates to the use of the proteins produced with these vectors in screening methods for identifying antibacterial substances and to the antibacterial substances found with these proteins.

French Abstract
L'invention concerne des acides nucleiques et leurs sequences proteiques derivees, qui possedent des fonctions essentielles a la vie d'Escherichia coli; des vecteurs et des cellules hotes, transformees au moyen desdits vecteurs, qui permettent l'expression desdites proteines essentielles et les proteines produites au moyen desdits vecteurs; ainsi que l'utilisation des proteines produites au moyen desdits vecteurs dans des techniques de criblage qui permettent de rechercher des substances antibacteriennes et les substances antibacteriennes trouvees au moyen desdites proteines.

German Abstract
Die Erfindung betrifft Nucleinsauren und davon abgeleitete Proteinsequenzen, die fur das Uberleben von Escherichia coli essentielle Funktionen besitzen. Sie umfasst daruber hinaus Vektoren und mit diesen transformierte Wirtszellen zur Expression solcher essentiellen Proteine sowie die mit diesen Vektoren erzeugten Proteine. Sie umfasst weiter die Verwendung der mit diesen Vektoren erzeugten Proteine in Screeningverfahren zur Auffindung antibakterieller Substanzen sowie der mit diesen Proteinen gefundenen antibakteriellen Substanzen.

3/3,AB/30 (Item 5 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT

00516310
i(STAPHYLOCOCCUS AUREUS) GENES AND POLYPEPTIDES
GENES ET POLYPEPTIDES DU STAPHYLOCOQUE DORE
Patent Applicant/Assignee:
HUMAN GENOME SCIENCES INC,
LUDWIG INSTITUTE FOR CANCER RESEARCH,
SIMPSON Andrew J G,
CHOI Gil H,
Inventor(s):
SIMPSON Andrew J G,
CHOI Gil H,
Patent and Priority Information (Country, Number, Date):
Patent: WO 9947662 A1 19990923
Application: WO 99US6199 19990318 (PCT/WO US9906199)
Priority Application: US 9878682 19980320; US 9880296 19980401; US 9884674 19980507
Designated States: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW GH GM KE LS MW SD SL SZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG
Publication Language: English
Fulltext Word Count: 32916

English Abstract
The present invention relates to 11 novel genes from i(S. aureus) and the polypeptides they encode. Also provided are vectors, host cells, antibodies and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of i(S. aureus) polypeptide activity. The invention additionally relates to diagnostic methods for detecting i(Staphylococcus) nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by i(Staphylococcus).

French Abstract

La presente invention concerne 11 genes issus du staphylocoque dore et les polypeptides qu'ils codent. L'invention concerne egalement des vecteurs, ces cellules hotes, des anticorps et des procedes a recombinaison permettant de les obtenir. L'invention concerne aussi des techniques de recherche systematique permettant d'identifier des agonistes et des antagonistes de l'activite polypeptide du staphylocoque dore. L'invention concerne en outre des techniques de diagnostic permettant de detecter dans un echantillon biologique des acides nucleiques, des polypeptides et des anticorps du staphylocoque dore. L'invention concerne enfin des vaccins permettant la prevention ou l'attenuation de l'infection par le staphylocoque.

3/3,AB/31 (Item 6 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT

00516287
i(STAPHYLOCOCCUS) AUREUS GENES AND POLYPEPTIDES
GENES ET POLYPEPTIDES DU i(STAPHYLOCCOCUS AUREUS)
Patent Applicant/Assignee:
HUMAN GENOME SCIENCES INC,
LUDWIG INSTITUTE FOR CANCER RESEARCH,
SIMPSON Andrew J G,
CHOI Gil H,
Inventor(s):
SIMPSON Andrew J G,
CHOI Gil H,
Patent and Priority Information (Country, Number, Date):
Patent: WO 9947639 A2 19990923
Application: WO 99US5976 19990319 (PCT/WO US9905976)
Priority Application: US 9878682 19980320; US 9880296 19980401; US 9884674 19980507
Designated States: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW GH GM KE LS MW SD SL SZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG
Publication Language: English
Fulltext Word Count: 34491

English Abstract
The present invention relates to 11 novel genes from i(S. aureus) and the polypeptides they encode. Also provided are vectors, host cells, antibodies and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of i(S. aureus) polypeptide activity. The invention additionally relates to diagnostic methods for detecting i(Staphylococcus) nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by i(Staphylococcus).

French Abstract
L'invention porte sur 11 nouveaux genes du i(Staphylococcus aureus), sur les polypeptides pour lesquels ils codent, et sur des vecteurs, des cellules hotes, des anticorps et des methodes de recombinaison pour les produire. L'invention porte en outre sur des methodes de criblage permettant d'identifier l'activite d'agonistes et d'antagonistes des polypeptides du i(Staphylococcus aureus), sur des procedes diagnostiques de detection des acides nucleiques, des polypeptides et des anticorps du i(Staphylococcus aureus) dans un echantillon biologique, et sur de nouveaux vaccins prevenant ou attenuant les infections par le i(Staphylococcus).

3/3,AB/32 (Item 7 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT

00466436
LIVE ATTENUATED VACCINES
VACCIN VIVANT ATTENUE
Patent Applicant/Assignee:
MEDICAL RESEARCH COUNCIL,
BALDWIN Thomas John,
BORRIELLO Saverio Peter,
PALMER Helen Mary,
Inventor(s):
BALDWIN Thomas John,
BORRIELLO Saverio Peter,
PALMER Helen Mary,
Patent and Priority Information (Country, Number, Date):
Patent: WO 9856901 A2 19981217
Application: WO 98GB1683 19980609 (PCT/WO GB9801683)
Priority Application: GB 9711964 19970609
Designated States: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW GH GM KE LS MW SD SZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG CI CM GA GN ML MR NE SN TD TG
Publication Language: English
Fulltext Word Count: 12457

English Abstract
An attenuated bacterium in which the native i(%fur%) %gene%, or homologue thereof, is modified such that the expression of the i(%fur%) %gene% product, or homologue thereof, is regulated independently of the iron concentration in the environment of the bacterium, is suitable for use as a live vaccine. The bacterium may be, in particular, i(%Neisseria% %meningitidis%).

French Abstract
On decrit une bacterie attenuee dans laquelle le gene i(fur) natif ou son homologue est modifie de sorte que l'expression du produit genique i(fur) ou son homologue est regulee independamment de la concentration en fer dans l'environnement de la bacterie. Cette bacterie attenuee peut etre utilisee en tant que vaccin vivant. De maniere plus specifique la bacterie peut etre i(%Neisseria% %meningitidis%).

3/3,AB/33 (Item 8 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT

00326885
DRUG FOR THE PREVENTION AND TREATMENT OF AUTO-IMMUNE AND VIRAL DISEASES, AND DIAGNOSTIC AGENTS FOR DETECTING SAID DISEASES
MEDICAMENT DESTINE A LA PROPHYLAXIE ET AU TRAITEMENT DE MALADIES AUTO-IMMUNES ET VIRALES, AGENTS DE DIAGNOSTIC POUR LE DEPISTAGE DESDITES MALADIES
Patent Applicant/Assignee:
MAX-PLANCK-GESELLSCHAFT ZUR FoRDERUNG DER WISSENSCHAFTEN E V,
MEYER Thomas Franz Ferdinand,
POHLNER Johannes,
BECK Susanne Christine,
JOSE Joachim,
WoLK Uwe,
LORENZEN Dirk R,
OETZELBERGER Karin Brigitte,
Inventor(s):
MEYER Thomas Franz Ferdinand,
POHLNER Johannes,
BECK Susanne Christine,
JOSE Joachim,
WoLK Uwe,

LORENZEN Dirk R,
OETZELBERGER Karin Brigitte,
Patent and Priority Information (Country, Number, Date):
Patent: WO 9609395 A2 19960328
Application: WO 95EP3726 19950921 (PCT/WO EP9503726)
Priority Application: DE 4433708 19940921
Designated States: AU CA JP US AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
Publication Language: German
Fulltext Word Count: 24171

English Abstract
The present invention concerne drugs and diagnostic agents as well as diagnostic, therapeutic and preventive methods for treating auto-immune and viral diseases in humans, these diseases being caused by pathogenic bacteria which are, in particular, micro-organisms colonizing human mucus membranes and secreting given exoproteins which display structural similarities to human proteins. Proteins similar to IgA protease which are absorbed particularly well by cells and present as antigens on MHC molecules are of particular significance in this respect. The IgA protease polyprotein (IPP) of pathogenic Neisseriae has a particularly marked homology to human proteins. For example, a given IPP peptide has marked homology to the articular proteins link and aggrekan. It is thus proven, for example, that the IPP is an etiological agent of rheumatoid arthritis (RA). The auto-immune reaction is further encouraged by other properties of the IPP-producing Neisseriae and IPPs. A particularly important property is the ability of the IPP to activate viruses and viral elements. This concerns in particular the activation of proviral retroviruses and endogenic retroviruses in humans. Further auto-immune reactions are induced in humans owing to the activation of viruses and viral elements. The development of acquired immune deficiency syndrome (AIDS) is also explained by the IPP-dependent activation of the HIV provirus. The properties according to the invention of the pathogenic Neisseriae and the IPPs formed thereby give rise to numerous novel diagnostic, therapeutic and preventive processes.

French Abstract
La presente invention concerne des medicaments et des agents de diagnostic, ainsi que des procedes diagnostiques, therapeutiques et prophylactiques pour le traitement de maladies auto-immunes et virales chez l'homme, lesdites maladies pouvant etre causees par des bacteries pathogenes. Ces bacteries sont, en particulier, des micro-organismes qui colonisent les muqueuses de l'homme et secretent certaines exoproteines presentant des similitudes structurelles avec les proteines humaines. Les proteines similaires a la protease IgA, qui sont particulierement bien absorbees par les cellules et se presentent sous forme d'antigenes sur les molecules de CMH, ont une importance particuliere dans ce contexte. La polyproteine de la protease IgA (IPP) de neisseria pathogenes presente une homologie particulierement marquee avec les proteines humaines. Par exemple, un peptide determine de l'IPP presente une homologie marquee avec les proteines articulaires de liaison et Aggrekan. Il est donc prouve, par exemple, que l'IPP est un agent etiologique de la polyarthrite rhumatoide (RA). La reaction auto-immune est en outre favorisee par d'autres proprietes des neisseria produisant l'IPP et des IPP. L'aptitude de l'IPP a activer les virus et les elements viraux constitue une propriete importante. Cela concerne en particulier l'activation de retrovirus proviraux et de retrovirus endogenes chez l'homme. D'autres reactions auto-immunes chez l'homme sont induites par l'activation de virus et d'elements viraux. En outre, le developpement du syndrome d'immunodeficience acquise (SIDA) s'explique egalement par l'activite du provirus VIH dependant de l'IPP. Les proprietes, decrites dans l'invention, des neisseria pathogenes et des IPP ainsi formees, permettent de developper de nombreux procedes diagnostiques, therapeutiques et prophylactiques nouveaux.

3/3,AB/34 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0233293 DBR Accession No.: 99-03394 PATENT
New attenuated bacterium containing a modified %fur% %gene% - live, attenuated %Neisseria% %meningitidis% or Neisseria gonorrhoeae preparation; ferric uptake regulation gene mutation for use as human infection vaccine
AUTHOR: Baldwin T J; Borriello S P; Palmer H M
CORPORATE SOURCE: London, UK.
PATENT ASSIGNEE: Med.Res.Counc. 1998
PATENT NUMBER: WO 9856901 PATENT DATE: 981217 WPI ACCESSION NO.: 99-080894 (9907)
PRIORITY APPLIC. NO.: GB 9711964 APPLIC. DATE: 970609
NATIONAL APPLIC. NO.: WO 98GB1683 APPLIC. DATE: 980609
LANGUAGE: English
ABSTRACT: A new attenuated bacterium contains a modified ferric uptake regulation (%fur%) %gene% , where the expressed product is regulated independently of iron concentration in the environment of the bacterium. Also claimed are: a %Neisseria% %meningitidis% strain having genotype aroB (or aroL) lac:fur fusion, recA or aroL (or aroB), galE, lac:fusion, recA; a preparation of membrane vesicles obtained from the bacterium; and a method for the preparation of the new bacterium. The bacterium may also be Neisseria gonorrhoeae and may be used to protect individuals against bacterial infection, e.g. meningococcal meningitis, stomach ulcers, gastric infections, whooping cough, and infection in an individual with cystic fibrosis. The bacterium also forms the basis of a method for preparing vaccines. Changing the regulation of the %fur% %gene% increases expression of important protective antigens during bacterial growth, which increases the efficiency of live vaccines administered to humans or animals. (49pp)

3/3,AB/35 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0220831 DBR Accession Number: 98-02428
Genetic and physiological characterization of the %fur% %gene% of Pseudomonas sp. KC - encoding carbon tetrachloride degradation (conference abstract)
AUTHOR: Knaebel D B; Lewis T A; Austin P R; Crawford R L
CORPORATE AFFILIATE: Univ.Clarkson Univ.Idaho
CORPORATE SOURCE: Clarkson University, Potsdam, NY 13699-5715, USA.
JOURNAL: Abstr.Gen.Meet.Am.Soc.Microbiol. (97 Meet., 354) 1997
ISSN: 0067-2777 CODEN: 0005P
CONFERENCE PROCEEDINGS: American Society for Microbiology, 97th General Meeting, Miami Beach, FL, 4-8 May, 1997.
LANGUAGE: English
ABSTRACT: Pseudomonas sp. KC is capable of carbon tetrachloride degradation to carbon dioxide with little production of chloroform. This ability appears to be related to iron and cobalt availability. The activity of the iron regulatory element Fur was studied so that information obtained could be used to understand the carbon tetrachloride degrading activity of Pseudomonas sp. KC. Polymerase chain reaction was used to amplify the coding region of the %fur% %gene% of Pseudomonas sp. KC. This was cloned into plasmid pBluescript SK+ and sequenced. It had a high degree of DNA sequence similarity to Pseudomonas aeruginosa (84%), Pseudomonas putida (81%), Bordetella pertussis (66%), Vibrio cholerae (65%) and Neisseria gonorrhoea and %Neisseria% %meningitidis% (both 63%). Based on presumptive amino acid sequences, the Pseudomonas sp. KC Fur showed 93% identity to P. putida Fur and 90% identity to P. aeruginosa Fur. The cloned Pseudomonas sp. KC fur was able to complement the Fur-Escherichia coli SBC796. It also produced a protein that cross-reacted with anti E. coli Fur antibody. (0 ref)

3/3,AB/36 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04274010 H.W. WILSON RECORD NUMBER: BGSA00024010
Iron metabolism in pathogenic bacteria.
Ratledge, Colin
Dover, Lynn G
Annual Review of Microbiology v. 54 (2000) p. 881-941
SPECIAL FEATURES: bibl diag tab ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 29223

ABSTRACT: The ability of pathogens to obtain iron from transferrins, ferritin, hemoglobin, and other iron-containing proteins of their host is central to whether they live or die. To combat invading bacteria, animals go into an iron-withholding mode and also use a protein (Nramp1) to generate reactive oxygen species in an attempt to kill the pathogens. Some invading bacteria respond by producing specific iron chelators--siderophores--that remove the iron from the host sources. Other bacteria rely on direct contact with host iron proteins, either abstracting the iron at their surface or, as with heme, taking it up into the cytoplasm. The expression of a large number of genes (>40 in some cases) is directly controlled by the prevailing intracellular concentration of Fe(II) via its complexing to a regulatory protein (the Fur protein or equivalent). In this way, the biochemistry of the bacterial cell can accommodate the challenges from the host. Agents that interfere with bacterial iron metabolism may prove extremely valuable for chemotherapy of diseases. Reprinted by permission of the publisher.

3/3,AB/37 (Item 2 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04050514 H.W. WILSON RECORD NUMBER: BGSA99050514
Contributions of genome sequencing to understanding the biology of Helicobacter pylori.
AUGMENTED TITLE: review
Ge, Zhongming
Taylor, Diane E
Annual Review of Microbiology v. 53 (1999) p. 353-87
SPECIAL FEATURES: bibl il ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 15698

ABSTRACT: About half of the world's population carries Helicobacter pylori, a gram-negative, spiral bacterium that colonizes the human stomach. The link between H. pylori and, ulceration as well as its association with the development of both gastric cancer and mucosa-associated lymphoid tissue lymphoma in humans is a serious public health concern. The publication of the genome sequences of two stains of H. pylori gives rise to direct evidence on the genetic diversity reported previously with respect to gene organization and nucleotide variability from strain to strain. The genome size of H. pylori strain 26695 is 1,6697,867 bp and is 1,643,831 bp for strain J99. Approximately 89% of the predicted open reading frames are common to both of the strains, confirming H. pylori as a single species. A region containing {similar}45% of H. pylori strain-specific open reading frames, termed the plasticity zone, is present on the chromosomes, verifying that some strain variability exists. Frequent alteration of nucleotides in the third position of the triplet codons and various copies of insertion elements on the individual chromosomes appear to contribute to distinct polymorphic fingerprints among strains analyzed by restriction fragment length polymorphisms, random amplified polymorphic DNA method, and repetitive element-polymerase chain reaction. Disordered chromosomal locations of some genes seen by pulsed-field gel electrophoresis are likely caused by rearrangement or inversion of certain segments in the genomes. Cloning and functional characterization of the genes involved in acidic survival, vacuolating toxin, cag-pathogenicity island, motility, attachment to epithelial cells, natural transformation, and the biosynthesis of lipopolysaccharides have considerably increased our

understanding of the molecular genetic basis for the pathogenesis of H. pylori. The homopolymeric nucleotide tracts and dinucleotide repeats, which potentially regulate the on- and off-status of the target genes by the strand-slipped mispairing mechanism, are often found in the genes encoding the outer-membrane proteins, in enzymes for lipopolysaccharide synthesis, and within DNA modification/restriction systems. Therefore, these genes may be involved in the H. pylori-host interaction. Reprinted by permission of the publisher.

3/3,AB/38 (Item 1 from file: 16)
DIALOG(R)File 16:Gale Group PROMT(R)

08927282 Supplier Number: 77416504
PART II Prescription for success.(pharmaceuticals in development)(Illustration)
News, Med Ad
Med Ad News, v20, n7, pNA
July, 2001
Language: English Record Type: Fulltext
Article Type: Illustration
Document Type: Magazine/Journal; Trade
Word Count: 34591

3/3,AB/39 (Item 1 from file: 135)
DIALOG(R)File 135:NewsRx Weekly Reports

0000115539 (USE FORMAT 7 OR 9 FOR FULLTEXT)
Iron-responsive regulator fur not essential in
Biotech Week, December 10, 2003, p.119

DOCUMENT TYPE: Expanded Reporting LANGUAGE: English
RECORD TYPE: FULLTEXT
WORD COUNT: 315
?

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Set     Items   Description
S1      57166   NEISSERIA (1W) MENINGITIDIS
S2         60   S1 AND FUR (1W) GENE
S3         39   RD (unique items)
? s s3 not py>1997
>>>One or more prefixes are unsupported
>>>  or undefined in one or more files.
Processing
Processed  10 of  60 files ...
Processing
Processed  20 of  60 files ...
Processing
Processing
Processed  30 of  60 files ...
Processing
Processed  40 of  60 files ...
Processing
Completed processing all files
              39  S3
        108100699  PY>1997
      S4      15  S3 NOT PY>1997
? t s4/3,ab/1-4
>>>No matching display code(s) found in file(s): 65, 107, 128-129, 135,
   229, 342, 345, 398, 429, 446-447, 449, 459, 761

 4/3,AB/1     (Item 1 from file: 73)
DIALOG(R)File  73:EMBASE
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05724381     EMBASE No: 1994118985
  Cloning and sequence analysis of the %fur% %gene% encoding an
iron-regulatory protein of %Neisseria% %meningitidis%
  Karkhoff-Schweizer R.R.; Schryvers A.B.; Schweizer H.P.
  Depart. Microbiol./Infectect. Dis., Univ. Calgary Hlth Sciences Center,
  3330 Hospital Drive N.W.,Calgary, Alta. T2N 4N1  Canada
  Gene ( GENE ) (Netherlands)  1994, 141/1 (139-140)
  CODEN: GENED   ISSN: 0378-1119
  DOCUMENT TYPE: Journal; Article
  LANGUAGE: ENGLISH   SUMMARY LANGUAGE: ENGLISH

  The %fur% %gene%, encoding an iron-regulatory protein in %Neisseria%
%meningitidis% strain B16B6, has been cloned and sequenced. Its product
showed a high degree of homology to known Fur sequences.


 4/3,AB/2     (Item 1 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)
(c) 2004 Inst for Sci Info. All rts. reserv.

05728818  References: 39
TITLE: IDENTIFICATION, CLONING, AND SEQUENCING OF A GENE REQUIRED FOR
    FERRIC VIBRIOBACTIN UTILIZATION BY VIBRIO CHOLERAE
AUTHOR(S): BUTTERTON JR; CALDERWOOD SB (Reprint)
CORPORATE SOURCE: MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114
  (Reprint); MASSACHUSETTS GEN HOSP,INFECT DIS UNIT/BOSTON//MA/02114;
  HARVARD UNIV,SCH MED,DEPT MICROBIOL & MOLEC GENET/BOSTON//MA/02115
PUBLICATION: JOURNAL OF BACTERIOLOGY, 1994, V176, N18 (SEP), P5631-5638
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ABSTRACT: Chromosomal DNA downstream of the Vibrio cholerae ferric
vibriobactin receptor gene, viuA, was cloned and sequenced, revealing an
813-bp open reading frame encoding a deduced protein of 271 amino acids. In
vitro transcription-translation of this DNA confirmed expression of a
protein of the expected size. A deletion mutation of this gene, viuB, was
created in the classical V. cholerae strain O395 by in vivo marker
exchange. By cross-feeding studies, this mutant was unable to utilize
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exogenous ferric vibriobactin but synthesized the siderophore normally; synthesis of siderophore by the mutant was also confirmed by the Arnow assay. Complementation of the mutant with a plasmid encoding only viuB restored ferric vibriobactin utilization to normal. Unexpectedly, hydropathicity analysis of ViuB did not reveal a signal sequence or transmembrane domain, suggesting that ViuB is not a periplasmic or membrane protein but may be a cytoplasmic protein involved in ferric vibriobactin uptake and processing, perhaps analogous to the Escherichia coli protein Fes. ViuB was not, however, homologous to Fes or to other proteins in the database. Complementation studies revealed that the cloned V. cholerae viuB gene could complement an E. coli fes mutant but that the cloned E. coli fes gene could not complement a V. cholerae viuB mutant; Northern (RNA) blot analysis of RNA from wild-type V. cholerae grown in high- and low-iron media revealed a monocistronic viuB message that was negatively regulated by iron at the transcriptional level. The promoter of viuB was located by primer extension and contained a nucleotide sequence highly homologous to the E. coli Fur binding consensus sequence, suggesting that expression of viuB is under the control of the V. cholerae %fur% %gene%.

4/3,AB/3 (Item 2 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)

05468121 References: 44
TITLE: CHARACTERIZATION OF THE VIBRIO CHOLERAE OUTER MEMBRANE HEME TRANSPORT PROTEIN HUTA - SEQUENCE OF THE GENE, REGULATION OF EXPRESSION, AND HOMOLOGY TO THE FAMILY OF TONB-DEPENDENT PROTEINS
AUTHOR(S): HENDERSON DP; PAYNE SM (Reprint)
CORPORATE SOURCE: UNIV TEXAS,DEPT MICROBIOL/AUSTIN//TX/78712 (Reprint); UNIV TEXAS,DEPT MICROBIOL/AUSTIN//TX/78712
PUBLICATION: JOURNAL OF BACTERIOLOGY, 1994, V176, N11 (JUN), P3269-3277
GENUINE ARTICLE#: NN851
ISSN: 0021-9193
LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The regulation of hutA, the Vibrio cholerae gene encoding a 77-kDa iron-regulated outer membrane protein required for heme iron utilization, was characterized, and the DNA sequence of the gene was determined. A hutA::Tn5 lac fusion generated previously (D. P. Henderson and S. M. Payne, Mel. Microbiol. 7:461-469, 1993) was transformed into Fur(-) and Fur(+) strains of Escherichia coli and V. cholerae. The results of beta-galactosidase assays on the transformed strains demonstrated that transcription of hutA is regulated by the Fur repressor protein in E. coil and at least partially regulated by Fur in V. cholerae. Analysis of the DNA sequence of hutA indicated that a sequence homologous to the E. coli consensus Fur box was present in the promoter region of hutA. The amino acid sequence of HutA is homologous to those of several TonB-dependent outer member proteins. However, when the V. cholerae heme utilization system, which requires one or more genes encoded by the recombinant plasmid pHUT10 in addition to hutA Carried on a second vector, was transferred to a wild-type strain and an isogenic tonB mutant of E. coli, the tonB mutant could utilize heme iron as efficiently as the wild-type strain. These data indicate that the V. cholerae heme utilization system reconstituted in E. coli does not require a functional TonB protein. The tonB mutant transformed with the heme utilization plasmids could not utilize the siderophore ferrichrome as an iron source, indicating that none of the genes encoded on the heme utilization plasmids complements the tonB defect in E. coli. It is possible that a gene(s) encoded by the recombinant heme utilization plasmids encodes a protein serving a TonB-like function in V. cholerae. A region in the carboxy terminus of HutA is homologous to the horse hemoglobin zeta chain, and the amino acids involved in forming the heme pocket in the zeta chain are conserved in HutA. These data suggest that this region of HutA is involved in heme binding.

4/3,AB/4 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

05375535 Genuine Article#: VU635 Number of References: 43
Title: IDENTIFICATION AND PURIFICATION OF A HEMOGLOBIN-BINDING OUTER-MEMBRANE PROTEIN FROM NEISSERIA-GONORRHOEAE (Abstract Available)
Author(s): CHEN CJ; SPARLING PF; LEWIS LA; DYER DW; ELKINS C
Corporate Source: UNIV N CAROLINA,SCH MED,DEPT MED/CHAPEL HILL//NC/27599; UNIV N CAROLINA,SCH MED,DEPT MED/CHAPEL HILL//NC/27599; UNIV OKLAHOMA,HLTH SCI CTR,DEPT MICROBIOL & IMMUNOL/OKLAHOMA CITY//OK/73190
Journal: INFECTION AND IMMUNITY, 1996, V64, N12 (DEC), P5008-5014
ISSN: 0019-9567
Language: ENGLISH Document Type: ARTICLE
Abstract: The majority of in vitro-grown Neisseria gonorrhoeae strains were unable to use hemoglobin as the sole source of iron for growth (Hgb(-)), but a minor population was able to do so (Hgb(+)), The ability of Hgb(+) gonococci to utilize hemoglobin as the iron source was associated with the expression of an iron-repressible 89-kDa hemoglobin-binding protein in the outer membrane. The N-terminal amino acid sequence of this protein revealed amino acids, from positions 2 to 16, identical to those of HpuB, an 85 kDa iron-regulated hemoglobin-haptoglobin utilization outer membrane protein of %Neisseria% %meningitidis%, Isogenic mutants constructed by allelic replacement with a meningococcal hpu::mini-Tn3erm construct no longer expressed the 89-kDa protein. Mutants could not utilize hemoglobin to support growth but still grew on heme. Thus, the gonococcal HpuB homolog is a functional hemoglobin receptor and is essential for growth with hemoglobin.
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